Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in this application. The following amendments do not constitute an admission regarding the patentability of the amended subject matter and should not be so construed. Applicant reserves the right to pursue the subject matter of the canceled claims in this or any other appropriate patent application.

Applicants withdraw from consideration claims 33-35, and 48-70 without prejudice to or disclaimer of the subject matter contained therein. Claims 31-32 and 36-47 are pending.

Listing of Claims:

Claims 1-30. (Cancelled)

31. (Previously presented) A method for determining at least one previously unidentified biological function of a target protein comprising:

(a) screening a multiplicity of different molecules for their ability to modify the stability of a target protein, wherein modification of the stability of said target protein by a molecule indicates that the molecule binds to said target protein;

(b) generating, from step (a), a first list of molecules that modify the stability of said target protein;

(c) comparing said first list from step (b) to at least one second list of molecules, wherein said second list of molecules are known to modify the stability of a group of proteins which share biological function; and

(d) determining if any molecule in said first list from step (b) is included in said second list from step (c), thereby determining at least one previously unidentified biological function of said target protein.

32. (Previously presented) The method of claim 31, wherein said screening step (a) comprises:

(a1) contacting said target protein with one or more of said multiplicity of different molecules in each of a multiplicity of containers;

(a2) treating said target protein in each of said multiplicity of containers to cause said target protein to unfold;

(a3) measuring in each of said containers a physical change associated with the unfolding of said target protein;

(a4) generating an unfolding curve for said target protein for each of said containers; and

(a5) comparing each of said unfolding curves in step (a4) to (1) each of said other unfolding curves and to (2) the unfolding curve obtained for said target protein in the absence of any of said multiplicity of different molecules; and

(a6) determining whether any of said multiplicity of different molecules modifies the stability of said target protein, wherein a modification in stability is indicated by a change in said unfolding curve.

33. Withdrawn

34. Withdrawn

35. Withdrawn

36. (Previously presented) A method for determining at least one previously unidentified biological function of a target protein comprising:

(a) screening a multiplicity of different molecules for their ability to shift the thermal unfolding curve of a target protein, wherein a shift in the thermal unfolding curve of said target protein by a molecule indicates that the molecule binds to said target protein;

(b) generating, from step (a), a first list of molecules that shift the thermal unfolding curve of said target protein;

(c) comparing said first list from step (b) to at least one second list of molecules, wherein said second list of molecules are known to modify the stability of a group of proteins which share biological function; and

(d) determining if any molecule in said first list from step (b) is included in said second list from step (c), thereby determining at least one previously unidentified biological function of said target protein.

37. (Previously presented) The method of claim 36, wherein said screening step (a) comprises:

(a1) contacting said protein with one or more of said multiplicity of different molecules in each of a multiplicity of containers;

(a2) heating said multiplicity of containers from step (a1);

(a3) measuring in each of said containers a physical change associated with the thermal unfolding of said target protein resulting from said heating;

(a4) generating a thermal unfolding curve for said target protein as a function of temperature for each of said containers; and

(a5) comparing each of said unfolding curve in step (a4) to (1) each of said other thermal unfolding curves and to (2) the thermal unfolding curve obtained for said protein in the absence of any of said multiplicity of different molecules; and

(a6) determining whether any of said multiplicity of different molecules shift the thermal unfolding curve of said protein.

38. (Previously presented) The method of claim 37, wherein said comparing step (a5) comprises ranking said molecules in said multiplicity of different molecules for binding to said target protein according to the ability of each of said multiplicity of different molecules to shift the thermal unfolding curve of said target protein.

39. (Previously presented) The method of claim 37, wherein in said heating step (a2), said multiplicity of containers is heated simultaneously.

40. (Previously presented) The method of claim 37, wherein said step (a4) further comprises determining a midpoint temperature (T_m) from the thermal unfolding curve; and

wherein said step (a5) further comprises comparing the T_m of each of said unfolding curves in step (a4) to (1) the T_m of each of said other thermal unfolding curves and to (2) the T_m of the thermal unfolding curve obtained for said target protein in the absence of any of said different molecules.

41. (Previously presented) The method of claim 37, wherein said step (a3) comprises measuring the absorbance of light by said contents of each of said containers.

42. (Previously presented) The method of claim 37, wherein said step (a1) comprises contacting said target protein with a fluorescence probe molecule present in each of said multiplicity of containers and wherein said step (a3) comprises

(i) exciting said fluorescence probe molecule, in each of said multiplicity of containers, with light; and

(ii) measuring the fluorescence from each of said multiplicity of containers.

43. (Previously presented) The method of claim 42, wherein said step (a3)(ii) further comprises measuring the fluorescence from each of said multiplicity of containers one container at a time.

44. (Previously presented) The method of claim 42, wherein said step (a3)(ii) further comprises measuring the fluorescence from a subset of said multiplicity of containers simultaneously.

45. (Previously presented) The method of claim 42, wherein said step (a3)(ii) further comprises measuring the fluorescence from each of said multiplicity of containers simultaneously.

46. (Previously presented) The method of claim 37, wherein said step (a3) comprises

(i) exciting tryptophan residues in said target protein, in each of said multiplicity of containers, with light; and

(ii) measuring the fluorescence from each of said multiplicity of containers.

47. (Previously presented) The method of claim 37, wherein said multiplicity of containers in step (a1) comprises a multiplicity of wells in a microplate.

Claims 48-70. Withdrawn